



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PATENT

In the Application of:

REBECCA E. CAHOON

ATTY. DOCKET NO.: BB-1201USDIV

APPLICATION NO.: 10/081,301

GROUP ART UNIT: 1652

FILED: FEBRUARY 20, 2002

EXAMINER: HUTSON, RICHARD G.

CONFIRMATION NO.: 2524

FOR: VITAMIN B METABOLISM
PROTEINS

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M.G.
1/15/03
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TECH CENTER 1600/2900

**SECOND PRELIMINARY AMENDMENT
AND RESPONSE TO RESTRICTION REQUIREMENT**

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

This is a Second Preliminary Amendment and Response to the Restriction Requirement set forth in the Office Action mailed December 6, 2002. Please enter the following:

IN THE SPECIFICATION:

Please amend the specification as follows; a marked-up version showing changes made is attached hereto:

Paragraph at page 6, line 19 through page 7, line 3:

C
A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or